GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 12:43:17 ; Search time 3 Seconds
(without alignments)
5.539 Million cell updates/sec

Title: US-10-035-958-60
Perfect score: 890
Sequence: 1 AAGTACTTGTGTCCGGGTGG.....TAAAAAAAAAAATCATCAAA 890

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 12 seqs, 9336 residues

Total number of hits satisfying chosen parameters: 24

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 12 summaries

Database : k035rng:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	865.7	97.3	909	1	AAC77539	Human ORFX ORF3094
2	858.9	96.5	903	1	AAA15582	Human phospholipid
3	858.9	96.5	903	1	ADK70378	Respiratory diseas
4	858.3	96.4	897	1	AAF94490	Human hydrophobic
5	784.3	88.1	826	1	AAX97660	Extended human sec
6	784.3	88.1	826	1	AAZ42252	Human phosphatidyl
7	664.7	74.7	681	1	AAF94480	Human hydrophobic
c 8	167.2	18.8	303	1	AAS62175	Porcine muscular s
c 9	120.2	13.5	133	1	AAH85783	Human single nucle
10	49.4001	5.6	686	1	ABT09032	Phase-1 Rat CT gen
11	48.8	5.5	1078	1	AAD42238	Corn FT homologue
12	48.2	5.4	1191	1	AAD42243	Corn FT homologue

ALIGNMENTS

RESULT 1
AAC77539
ID AAC77539 standard; cDNA; 909 BP.
XX
AC AAC77539;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF3094 polynucleotide sequence SEQ ID NO:6187.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX
PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR P-PSDB; AAB43330.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 5; Page 5369-5370; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 909 BP; 232 A; 254 C; 236 G; 186 T; 0 U; 1 Other;

Query Match 97.3%; Score 865.7; DB 1; Length 909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 881; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

```
Qy          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||
Db         12 AAGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCC 71

Qy         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 131

Qy        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 191
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Qy        181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 251

Qy        241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 311

Qy        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        312 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGTACGGCGCAACCTATAT 371

Qy        361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 431

Qy        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 491

Qy        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 551

Qy        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 611

Qy        601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        612 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGC 671

Qy        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGA 731

Qy        721 AAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGG 779
              |||||||||||||||||||||| ||||||||| |||||||||||||||||||||||||
Db        732 AAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGG 791

Qy        780 CTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCC 839
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        792 CTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCC 851

Qy        840 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAA 889
              |||||||||||||||||||||||||||||||||||||||||||||| |
Db        852 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCCA 901
```

RESULT 2
AAA15582
ID AAA15582 standard; cDNA; 903 BP.
XX
AC AAA15582;
XX
DT 01-AUG-2000 (first entry)
XX
DE Human phospholipid binding protein 2, PLBP2 gene.
XX
KW Human; phospholipid binding protein; PLBP2; foetal development disorder;
KW reproduction disorder; cell proliferation disorder; immune response;
KW autoimmune disorder; AIDS; infertility; cytostatic; immunosuppressive;
KW gene therapy; hereditary neuropathy;
KW phosphatidylethanolamine binding protein D1; PE-BP D1; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   88. .771
FT   /*tag= a
FT   /product= "Human PLBP2"
XX

PN US6063767-A.
XX
PD 16-MAY-2000.
XX
PF 09-DEC-1998; 98US-00208718.
XX
PR 28-OCT-1997; 97US-00958820.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Corley NC, Shah P, Lal P, Hillman JL;
XX
DR WPI; 2000-375529/32.
DR P-PSDB; AAY94263.
XX
PT New purified phospholipid binding proteins 1 and 2 useful for diagnosing,
PT treating or preventing diseases disorders associated with fetal
PT development, reproduction, cell proliferation, and the immune response.
XX
PS Example 5; Fig 2; 37pp; English.
XX
CC The present sequence is the phospholipid binding protein 2 (PLBP2) gene.
CC This gene is expressed in lung, prostate and heart tissues. Also, the
CC protein is expressed in foetal tumour tissues. PLBP2 may be used for the
CC diagnosis, prevention, or treatment of disorders associated with foetal
CC development (e.g. hereditary neuropathies), reproduction (e.g.
CC infertility), cell proliferation (e.g. cancers), and the immune response
CC (AIDS). PLBP2 antibodies may also be developed for potential drug
CC screening or to quantitate PLBP2 gene expression in biopsied tissues. The
CC PLBP2 gene may be administered for gene therapy of disorders associated
CC with PLBP2. PLBP2 has high homology with the phosphatidylethanolamine
CC binding protein D1, PE-BP D1, of Onchocerca volvulus. PE-BP DI is thought
CC to play a role in transport or signal mechanisms between membranes and
CC the cytoplasm
XX
SQ Sequence 903 BP; 222 A; 251 C; 242 G; 188 T; 0 U; 0 Other;

Query Match 96.5%; Score 858.9; DB 1; Length 903;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 873; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```
Qy          2 AGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCT 61
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||| ||||
Db          1 AGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCT 60

Qy         62 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 120

Qy        122 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 180

Qy        182 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 240

Qy        242 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 300

Qy        302 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 360

Qy        362 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 420

Qy        422 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAG 481
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        421 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAG 480
```

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Qy        482 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 540

Qy        542 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 600

Qy        602 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 660

Qy        662 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 720

Qy        722 AGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780
              |||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||||
Db        721 AGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        781 TTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCC 840

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAA 880
              |||||||||||||||||||||||||| |||||||||
Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAAA 880
```

RESULT 3
ADK70378
ID ADK70378 standard; cDNA; 903 BP.
XX
AC ADK70378;
XX
DT 06-MAY-2004 (first entry)
XX
DE Respiratory disease differentially expressed cDNA #114.
XX
KW ds; gene; cytostatic; respiratory; antiasthmatic; gene therapy;
KW differential gene expression; respiratory disorder; lung cancer;
KW chronic obstructive pulmonary disease; emphysema; asthma.
XX
OS Homo sapiens.
XX
PN WO2003101283-A2.
XX
PD 11-DEC-2003.
XX
PF 02-JUN-2003; 2003WO-US017409.
XX
PR 04-JUN-2002; 2002US-0386005P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Rickert PK, Krasnow R;
XX
DR WPI; 2004-042945/04.
XX
PT New combination comprising cDNAs and proteins that are differentially
PT expressed in respiratory disorders, useful for diagnosing or treating
PT respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
PT diseases or asthma.
XX
PS Claim 1; SEQ ID NO 114; 343pp; English.
XX
CC The invention relates to cDNA sequences that are differentially expressed
CC in respiratory disorders or their complements or encoded proteins. The
CC cDNAs and proteins are useful for diagnosing, treating or monitoring
CC treatment of a subject with a respiratory disease including lung cancer,
CC chronic obstructive pulmonary diseases, emphysema or asthma. The protein
CC is also useful for screening molecules or compounds to identify at least
CC one ligand which specifically binds the protein. It is also useful for
CC preparing and purifying a polyclonal or monoclonal antibody. This
CC sequence corresponds to a cDNA of the invention.
XX
SQ Sequence 903 BP; 222 A; 251 C; 242 G; 188 T; 0 U; 0 Other;

  Query Match   96.5%; Score 858.9; DB 1; Length 903;
  Best Local Similarity   99.2%; Pred. No. 0;
  Matches 873; Conservative   0; Mismatches   6; Indels   1; Gaps   1;

```
Qy          2 AGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCT 61
              |||||||||||||||||||||||||||| |||||||||||||||||||||||| ||||
Db          1 AGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCT 60

Qy         62 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 120

Qy        122 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 180

Qy        182 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 240

Qy        242 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 300

Qy        302 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 360

Qy        362 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 420

Qy        422 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAG 481
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        421 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAG 480

Qy        482 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 540

Qy        542 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 600

Qy        602 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 660

Qy        662 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 720

Qy        722 AGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780
              |||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||||
Db        721 AGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        781 TTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCC 840

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAA 880
              |||||||||||||||||||||||||| |||||||||
Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAAA 880
```

RESULT 4
AAF94490
ID AAF94490 standard; cDNA; 897 BP.

XX
AC AAF94490;
XX
DT 04-JUN-2001 (first entry)
XX
DE Human hydrophobic domain containing protein clone HP03880 cDNA #114.
XX
KW Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
KW antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory;
KW cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW behavioural characteristic; immune response; ss.
XX
OS Homo sapiens.
XX
PN WO200112660-A2.
XX
PD 22-FEB-2001.
XX
PF 10-AUG-2000; 2000WO-JP005356.
XX
PR 17-AUG-1999; 99JP-00230344.
PR 07-SEP-1999; 99JP-00252551.
PR 01-OCT-1999; 99JP-00281132.
PR 22-OCT-1999; 99JP-00301624.
PR 04-NOV-1999; 99JP-00313877.
XX
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2001-160059/16.
DR P-PSDB; AAB88590.
XX
PT Human proteins with hydrophobic domains and the DNAs which encode them
PT are useful for treating autoimmune disorders, burns and tumors and for
PT screening novel pharmaceuticals.
XX
PS Claim 4; Page 442-444; 518pp; English.
XX
CC AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
CC AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
CC anti-HIV, neuroprotective, antianaemic, vulnerary, antiulcer,
CC osteopathic, anti-inflammatory and cytostatic activities, and can be used
CC in gene therapy. (I) can be used as pharmaceuticals and as antigens to
CC prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
CC for genetic diagnosis and gene sources for gene therapy or for producing
CC (I) in large quantities. Cells containing (II) are used for the detection
CC of ligands or receptors corresponding to membrane or secretory proteins
CC and to screen small molecule novel pharmaceuticals. Antibodies directed
CC to (I) can be used for the detection, quantification and purification of
CC (I). Activities of (I) may include cytokine and cell
CC proliferation/differentiation function, immune stimulating or suppressing
CC activity, haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory
CC activity. (I) and (II) can be used to treat autoimmune disorders e.g.
CC multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
CC inflammatory bowel disease and tumours. (I) and (II) can also be used for
CC wound healing, as nutritional sources or supplements e.g. as amino acid,
CC carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
CC processing and utilisation of dietary fat, protein, carbohydrate,
CC vitamins and minerals, to effect behavioural characteristics, to affect
CC appetite, and can act as antigens in vaccines to raise an immune response
CC to the protein or another material cross-reactive with the protein
XX
SQ Sequence 897 BP; 226 A; 253 C; 234 G; 184 T; 0 U; 0 Other;

Query Match 96.4%; Score 858.3; DB 1; Length 897;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 873; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```
Qy    1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
Db   11 AAGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCC 70

Qy   61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120
Db   71 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 130

Qy  121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
Db  131 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 190

Qy  181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
Db  191 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 250

Qy  241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
Db  251 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 310

Qy  301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
Db  311 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 370

Qy  361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
Db  371 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 430

Qy  421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
Db  431 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 490

Qy  481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
Db  491 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 550

Qy  541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
Db  551 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 610

Qy  601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660
Db  611 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGC 670

Qy  661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
Db  671 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGA 730

Qy  721 AAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGG 779
Db  731 AAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGG 790

Qy  780 CTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCC 839
Db  791 CTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCC 850

Qy  840 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAA 880
Db  851 CTCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAAA 891
```

RESULT 5
AAX97660
ID AAX97660 standard; DNA; 826 BP.
XX
AC AAX97660;
XX
DT 13-SEP-1999 (first entry)
XX
DE Extended human secreted protein coding sequence, SEQ ID NO. 124.
XX
KW Secreted protein; human; cytokine; cellular proliferation; cell movement;

KW cellular differentiation; immune system regulator; anti-inflammatory;
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO9931236-A2.
XX
PD 24-JUN-1999.
XX
PF 17-DEC-1998; 98WO-IB002122.
XX
PR 17-DEC-1997; 97US-0069957P.
PR 09-FEB-1998; 98US-0074121P.
PR 13-APR-1998; 98US-0081563P.
PR 10-AUG-1998; 98US-0096116P.
XX
PA (GEST) GENSET.
XX
PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX
DR WPI; 1999-385906/32.
DR P-PSDB; AAY35976.
XX
PT New isolated human secreted proteins.
XX
PS Claim 1; Page 255; 516pp; English.
XX
CC This sequence represents an extended human secreted protein coding
CC sequence of the invention. The secreted proteins can be used in treating
CC or controlling a variety of human conditions. The secreted proteins may
CC act as cytokines or may affect cellular proliferation or differentiation
CC or may act as immune system regulators, haematopoiesis regulators, tissue
CC growth regulators, regulators of reproductive hormones or cell movement
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC tumour inhibition activity. The DNAs can be used in forensic procedures
CC to identify individuals or in diagnostic procedures to identify
CC individuals having genetic diseases resulting from abnormal expression of
CC the genes corresponding to the extended cDNAs. They are also useful for
CC constructing a high resolution map of the human chromosomes. They can
CC also be used for gene therapy to control or treat genetic diseases
XX
SQ Sequence 826 BP; 228 A; 229 C; 211 G; 158 T; 0 U; 0 Other;

Query Match 88.1%; Score 784.3; DB 1; Length 826;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```
Qy         75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 60

Qy        135 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCT 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCC 120

Qy        195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 180

Qy        255 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 240

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 300

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 360

Qy        435 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 420

Qy        495 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 480

Qy        555 TTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 614
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCAGGAAGGAAAGGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 540

Qy        615 AAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 674
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        541 AAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 600

Qy        675 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGC 734
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        601 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGC 660

Qy        735 CCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 793
              |||||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        661 CCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 720

Qy        794 CATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 853
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        721 CATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 780

Qy        854 CCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||| |||||||||
Db        781 CCCCTTCTTTTCCAAATAAAAAAAAA 807
```

RESULT 6
AAZ42252
ID AAZ42252 standard; cDNA; 826 BP.
XX
AC AAZ42252;
XX
DT 01-FEB-2000 (first entry)
XX
DE Human phosphatidylethanolamine-binding protein encoding cDNA.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
KW location; development; protein synthesis; stability; regulation;
KW identification; ss.
XX
OS Homo sapiens.
XX
PN WO9953051-A2.
XX
PD 21-OCT-1999.
XX
PF 09-APR-1999; 99WO-IB000712.
XX
PR 09-APR-1998; 98US-00057719.
PR 28-APR-1998; 98US-00069047.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-038446/03.
DR P-PSDB; AAY64647.
XX
PT Novel secreted protein 5' expressed sequence tag sequences used in
PT diagnostic, forensic, gene therapy, and chromosome mapping procedures.
XX
PS Example 21; Page 168-169; 837pp; English.
XX
CC AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
CC sequences, corresponding to human secreted proteins. AAY64651 to AAY65438

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CC   represent the EST-related proteins corresponding to AAZ42265 to AAZ43052.
CC   The 5' ESTs can be used for producing secreted human gene products. They
CC   can be used to identify and isolate 5' untranslated regions (UTRs) and
CC   upstream regulatory regions which control the location, development
CC   stage, rate, and quantity of protein synthesis, as well as stability of
CC   mRNA. The ESTs are also useful as probes for chromosome mapping, and to
CC   obtain full length cDNA clones. The ESTs can also be used in forensic
CC   procedures to identify individuals, or in diagnostic procedures to
CC   identify individuals having genetic diseases resulting from abnormal gene
CC   expression. The products may also be used in gene therapy protocols. The
CC   nucleic acids encoding signal peptides can be used for directing
CC   extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell. The
CC   proteins encoded by the EST sequences may be useful in treating a variety
CC   of human conditions. Secreted proteins have therapeutic value, and the
CC   identification of new secreted proteins is valuable. AAZ42249 to AAZ42264
CC   and AAY64644 to AAY64650 represent sequences used in the exemplification
CC   of the present invention
XX
SQ   Sequence 826 BP; 228 A; 229 C; 211 G; 158 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 784.3;  DB 1;  Length 826;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy         75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 60

Qy        135 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCT 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCC 120

Qy        195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 180

Qy        255 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 240

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 300

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 360

Qy        435 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 420

Qy        495 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 480

Qy        555 TTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 614
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCAGGAAGGAAAGGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 540

Qy        615 AAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 674
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        541 AAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 600

Qy        675 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGC 734
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        601 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGC 660

Qy        735 CCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 793
              |||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        661 CCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 720

Qy        794 CATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 853
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 780

Qy        854 CCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||| |||||||||
Db        781 CCCCTTCTTTTCCAAATAAAAAAAAA 807


RESULT 7
AAF94480
ID   AAF94480 standard; cDNA; 681 BP.
XX
AC   AAF94480;
XX
DT   04-JUN-2001  (first entry)
XX
DE   Human hydrophobic domain containing protein clone HP03880 cDNA #104.
XX
KW   Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
KW   antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory;
KW   cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
KW   HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW   inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW   behavioural characteristic; immune response; ss.
XX
OS   Homo sapiens.
XX
PN   WO200112660-A2.
XX
PD   22-FEB-2001.
XX
PF   10-AUG-2000; 2000WO-JP005356.
XX
PR   17-AUG-1999;   99JP-00230344.
PR   07-SEP-1999;   99JP-00252551.
PR   01-OCT-1999;   99JP-00281132.
PR   22-OCT-1999;   99JP-00301624.
PR   04-NOV-1999;   99JP-00313877.
XX
PA   (SAGA ) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
XX
PI   Kato S,  Kimura T;
XX
DR   WPI; 2001-160059/16.
DR   P-PSDB; AAB88590.
XX
PT   Human proteins with hydrophobic domains and the DNAs which encode them
PT   are useful for treating autoimmune disorders, burns and tumors and for
PT   screening novel pharmaceuticals.
XX
PS   Claim 3; Page 426-427; 518pp; English.
XX
CC   AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
CC   AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
CC   anti-HIV, neuroprotective, antianaemic, vulnerary, antiulcer,
CC   osteopathic, anti-inflammatory and cytostatic activities, and can be used
CC   in gene therapy. (I) can be used as pharmaceuticals and as antigens to
CC   prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
CC   for genetic diagnosis and gene sources for gene therapy or for producing
CC   (I) in large quantities. Cells containing (II) are used for the detection
CC   of ligands or receptors corresponding to membrane or secretory proteins
CC   and to screen small molecule novel pharmaceuticals. Antibodies directed
CC   to (I) can be used for the detection, quantification and purification of
CC   (I). Activities of (I) may include cytokine and cell
CC   proliferation/differentiation function, immune stimulating or suppressing
CC   activity, haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity and anti-inflammatory
CC   activity. (I) and (II) can be used to treat autoimmune disorders e.g.
CC   multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
CC   inflammatory bowel disease and tumours. (I) and (II) can also be used for
```

```
CC   wound healing, as nutritional sources or supplements e.g. as amino acid,
CC   carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
CC   processing and utilisation of dietary fat, protein, carbohydrate,
CC   vitamins and minerals, to effect behavioural characteristics, to affect
CC   appetite, and can act as antigens in vaccines to raise an immune response
CC   to the protein or another material cross-reactive with the protein
XX
SQ   Sequence 681 BP; 179 A; 186 C; 183 G; 133 T; 0 U; 0 Other;

  Query Match             74.7%;  Score 664.7;  DB 1;  Length 681;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches  677;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         89 ATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGATGGTGGTC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGATGGTGGTC 60

Qy        149 ACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGAGGACACC 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGAGGACACC 120

Qy        209 CTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGGTT 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGGTT 180

Qy        269 GTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAG 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAG 240

Qy        329 TTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCT 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCT 300

Qy        389 AGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGC 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGC 360

Qy        449 GCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCC 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCC 420

Qy        509 CCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAA 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAA 480

Qy        569 GTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTT 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTT 540

Qy        629 CTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTAC 688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTAC 600

Qy        689 CAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCAC-AAAAC 747
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCACAAAAAC 660

Qy        748 CAGGCAGAGATAGCTGCCTGC 768
              |||||||||||||||||||||
Db        661 CAGGCGGAGATAGCTGCCTGC 681


RESULT 8
AAS62175/c
ID   AAS62175 standard; cDNA; 303 BP.
XX
AC   AAS62175;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Porcine muscular steatosis-modulating factor #301.
XX
KW   Pig; muscular steatosis-modulating factor; ss; metabolic; muscular; MSMF;
KW   food supplement; obesity; hyperlipidaemia; atherosclerosis;
KW   wound healing; tumour; amyotrophic lateral sclerosis; ALS.
XX
OS   Sus scrofa.
XX
PN   WO200179287-A2.
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-CA000509.
XX
PR   17-APR-2000; 2000US-0197936P.
XX
PA   (MIAC ) CANADA AGRIC & AGRI-FOOD CANADA.
XX
PI   Palin M,  Pomar C,  Gariepy C;
XX
DR   WPI; 2002-017600/02.
XX
PT   Prognosis and diagnosis of muscular steatosis, useful e.g. for selecting
PT   animals for breeding, by measuring levels of specific markers, also
PT   treating or inducing steatosis.
XX
PS   Claim 5; Page 188-189; 190pp; English.
XX
CC   The invention relates to prognosis or diagnosis of muscular steatosis by
CC   measuring the level of a muscular steatosis modulating factor (MSMF) in a
CC   human or animal and comparing this with the level in a healthy control.
CC   Any difference indicates presence of, or predisposition to, muscular
CC   steatosis. The method is particularly used for diagnosis or prognosis of
CC   muscular steatosis in mammals and birds, e.g. to select individuals as
CC   founders in animal breeding. Also (ant)agonists of MSMF can be used to
CC   treat, or induce (for increasing the fat content of food) muscular
CC   steatosis, in humans and animals. The MSMF markers are also useful in the
CC   study of diseases and conditions such as obesity, hyperlipidaemia,
CC   atherosclerosis, wound healing, tumours and amyotrophic lateral sclerosis
CC   (ALS). The present sequence is a MSMF of the invention
XX
SQ   Sequence 303 BP; 59 A; 72 C; 87 G; 82 T; 0 U; 3 Other;

  Query Match             18.8%;  Score 167.2;  DB 1;  Length 303;
  Best Local Similarity   80.1%;  Pred. No. 0;
  Matches  229;  Conservative    0;  Mismatches   51;  Indels    6;  Gaps    3;

Qy        536 TACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAAC 595
              ||||||||||| |  ||| |||| | ||||||  ||||||||||||||||||| ||||||
Db        303 TACCAGTTCTTNGNNTATGTTCA-GCAGGAAAGAGCATCTCTCTCCTTCCCAAAGAAAAC 245

Qy        596 AAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCT 655
              |||||||||| |||||||||||||| |||||||| |||||||||||| ||||||||
Db        244 AAAACTCGAGGTTCTTGGAAAATGGACAAATTTCTGAGCCGCTTCCACCTGAGCGAACCT 185

Qy        656 GAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCC 715
              ||||| |||||||||||||||||| | |||||||||||| ||  |||||| |
Db        184 GAAGCCAGCACCCAGTTCATGACCCAGTATTACCAGGACTCACAAAAGCTCCAGCCAGGG 125

Qy        716 AGAGGAAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAG 775
              ||||||    || ||||||||| ||||| ||| || |||||| ||||| || |||
Db        124 GAAGGAAG---TAGTGAGCCCAAGGACAAACCCAAGCGGAGATAACTGCCCGCCAGACCT 68

Qy        776 CCGGCTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACG 821
              | |||||  |  | | ||  |||| | ||| |||||||| ||  ||
Db         67 CAGGCTTCACGTTGCAGG--TGTGTCTACAGTGCTCACCGCCCTCG 24


RESULT 9
AAH85783/c
ID   AAH85783 standard; DNA; 133 BP.
XX
AC   AAH85783;
XX
DT   27-FEB-2002  (first entry)
XX
```

DE Human single nucleotide polymorphism containing DNA sequence #640.
XX
KW Biallelic marker; polymorphism; human; disease; diagnosis; treatment;
KW phenotypic trait; gene therapy; forensic; paternity; mapping; cancer;
KW transgenic; single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(59,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9953095-A2.
XX
PD 21-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US006893.
XX
PR 09-APR-1998; 98US-00057871.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Lander ES, Wang D, Hudson T;
XX
DR WPI; 1999-620443/53.
XX
PT Polymorphic human genomic sequences and related allele-specific probes
PT and primers, useful for genetic analysis, e.g. diagnosis and monitoring
PT of disease.
XX
PS Claim 1; Page 99; 330pp; English.
XX
CC This invention describes novel human nucleic acid segments (I) containing
CC polymorphic sites. The polynucleotides of (I) are used for, e.g.
CC correlating disease polymorphisms (or disease susceptibility) or other
CC phenotypic traits (e.g. baldness, obesity, fertility, strength, response
CC to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation,
CC heart or central nervous system diseases; detecting susceptibility to
CC microbial infection; treating or preventing such diseases; forensic
CC analysis; gene therapy; paternity testing; mapping genomic loci
CC associated with phenotypic traits (and subsequent cloning of the genes
CC responsible); and the production of transgenic organisms. Antibodies
CC raised against (I) are useful as diagnostic and therapeutic tools and in
CC drug screening. AAH85144 - AAH87644 represent the human DNA sequences
CC containing biallelic polymorphic sites described in the invention
XX
SQ Sequence 133 BP; 25 A; 31 C; 43 G; 33 T; 0 U; 1 Other;

Query Match 13.5%; Score 120.2; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 122; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy        743 AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCC 802
              |||||||||| |||||||||||||||||||||| | ||||||||||||||||||||||||
Db        126 AAAACCAGGCGGAGATAGCTGCCTGCTAGATAGNCCGCTTTGCCATCCGGGCATGTGGCC 67

Qy        803 ACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTT 862
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTT 7

Qy        863 TTCCAA 868
              ||||||
Db          6 TTCCAA 1
```

RESULT 10
ABT09032
ID ABT09032 standard; DNA; 686 BP.
XX
AC ABT09032;
XX
DT 05-DEC-2002 (first entry)
XX
DE Phase-1 Rat CT gene SEQ ID No 120.
XX
KW Rat; toxicity study; rat toxic response gene; toxicological response;
KW drug development; phase-1 rat CT gene; ds.
XX
OS Rattus sp.
XX
PN WO200266682-A2.
XX
PD 29-AUG-2002.
XX
PF 29-JAN-2002; 2002WO-US002935.
XX
PR 29-JAN-2001; 2001US-0264933P.
PR 26-JUL-2001; 2001US-0308161P.
XX
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI Farris G, Hicken SH, Farr SB;
XX
DR WPI; 2002-674961/72.
XX
PT Evaluating the toxicity of an agent, useful in drug development or in
PT determining toxicological responses to a new drug, by determining the
PT expression of rat toxicologically relevant genes in the test animal in
PT response to the test agent.
XX
PS Disclosure; Page 135; 388pp; English.
XX
CC The invention relates to a method used for evaluating the toxicity of an
CC agent comprising determining the expression of a rat toxic response
CC gene(s) in the test animal in response to the agent. The method is useful
CC in drug development, particularly for conducting toxicity studies and
CC analysis before a new drug or compound is approved for human consumption
CC or use. The method is also useful in determining toxicological responses
CC to a new drug. This polynucleotide sequence represents a phase-1 rat CT
CC gene of the invention
XX
SQ Sequence 686 BP; 159 A; 200 C; 203 G; 123 T; 0 U; 1 Other;

Query Match 5.6%; Score 49.4001; DB 1; Length 686;
Best Local Similarity 48.8%; Pred. No. 0;
Matches 181; Conservative 0; Mismatches 166; Indels 24; Gaps 2;

```
Qy        355 CTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATT 414
              ||| | ||||||  |    || || ||||| || |||||    || |||| |   ||
Db        218 CTACACCCTGGTCCTCACAGACCCCGATGCTCCCAGCAGGAAGGACCCCAAATTCAGGGA 277

Qy        415 CTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCA 474
              |||   || | |||||     | || ||||||  |||| | |  |  || |   | |
Db        278 GTGGCACCACTTCCTGGTGGTCAACATGAAGGGCAACGACATTAGCAGTGGCACTGTCC- 336

Qy        475 GGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCG 534
              |  || |  |||  ||   ||   || ||   | |||  ||  | | ||  ||
Db        337 ----------TCTCCGAATACGTGGGCTCCGGACCTCCCAAAGACACAGGTCTGCACCG 385

Qy        535 CTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAA 594
              ||||   |   | || |||  |||||         | | || |  |  ||||    |
Db        386 CTACGTCTGGCTGGTGTATGAGCAGGAGCAGCCTCTGAACTGTGACGAGCCCATCCTCAG 445

Qy        595 CAAAACT----------CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCA 642
              ||| |             || |||   |  ||  ||||    || |  ||    | |||
Db        446 CAACAAGTCTGGAGACAACCGCGGCAAGTTCAAGGTGGAGTCCTTCCGCAAGAAGTACCA 505

Qy        643 CCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAAC 702
              |||||| |  || |  ||  ||||    |||  | |  ||    | |         ||| |
Db        506 CCTGGGAGCCCCGGTGGCCGGCACGTGCTTCCAGGCAGAGTGGGATGACTCTGTGCCCAA 565

Qy        703 CCTCCAGGCTC 713
              || || | ||
Db        566 GCTGCATGATC 576
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```
RESULT 11
AAD42238
ID   AAD42238 standard; cDNA; 1078 BP.
XX
AC   AAD42238;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Corn FT homologue cDNA #1.
XX
KW   Floral developmental protein; flowering locus T; APETALA3; transgenic;
KW   FT; AP3; transgenic plant; fertility; flower development; gene mapping;
KW   sterility; plant growth; inflorescence architecture; plant morphology;
KW   tissue culture; cell division; corn; gene; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             312. .833
FT                   /*tag=  a
FT                   /product= "Corn FT homologue protein"
XX
PN   WO200244390-A2.
XX
PD   06-JUN-2002.
XX
PF   21-NOV-2001; 2001WO-US043750.
XX
PR   28-NOV-2000; 2000US-0253415P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon EB,  Cahoon RE,  Klein TM,  Rafalski AJ,  Sakai H;
XX
DR   WPI; 2002-547703/58.
DR   P-PSDB; AAE25736.
XX
PT   New floral developmental polypeptide having flowering locus T or Ap3
PT   homolog activity, useful for immunological screening of cDNA expression
PT   libraries.
XX
PS   Claim 6; Page 54; 88pp; English.
XX
CC   The present invention relates to novel floral developmental proteins,
CC   more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
CC   proteins and polynucleotides encoding such proteins. Floral developmental
CC   polynucleotides are useful for transforming cells or for producing plants
CC   by transforming the plant cells with the polynucleotides and regenerating
CC   the plants from the transformed plant cells. Sequences of the invention
CC   are useful for immunological screening of cDNA expression libraries. They
CC   are also useful for creating transgenic plants. Polynucleotides of the
CC   invention are used as probes for genetically and physically mapping the
CC   genes that they are a part of and as markers for traits linked to those
CC   genes. AP3 homologues may be useful for engineering plant sterility or
CC   fertility, flower development and morphology. FT or TFL1 homologues are
CC   useful for engineering flowering time, plant growth rate, inflorescence
CC   architecture, tissue culture morphology and rate of cell division to
CC   enhance transformation. The present sequence is corn FT homologue cDNA
CC   from a contig of clones cbn10.pk0052.f5, cbn2.pk0035.f12,
CC   cco1n.pk0010.h3, p0095.cwsas14f, p0119.cmtmg45rb and p0128.cpicl42r
XX
SQ   Sequence 1078 BP; 197 A; 336 C; 321 G; 224 T; 0 U; 0 Other;

  Query Match             5.5%;  Score 48.8;  DB 1;  Length 1078;
  Best Local Similarity   50.9%;  Pred. No. 0;
  Matches  138;  Conservative    0;  Mismatches  127;  Indels    6;  Gaps    1;

Qy        182 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 241
Db        318 CGTGGGGATCCGCTGGTGGTGGGCCGCATCATCGGCGACGTGGTGGACCCCTTCGTGCGC 377

Qy        242 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 301
Db        378 CGGGTGCCGCTCCGCGTCGCCTACGCCGCGCGCGAGGTCTCCAACGGCTGCGAGCTCAGG 437

Qy        302 ACCTCCTGGATGG------AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACC 355
Db        438 CCCTCCGCCATCGCCGACCAGCCGCGCGTCGAGGTCGGCGGACCCGACATGCGCACCTTC 497

Qy        356 TATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTC 415
Db        498 TACACCCTCGTGATGGTAGATCCTGATGCGCCGAGCCCCAGCGATCCCAACCTCAGGGAG 557

Qy        416 TGGAGACATTGGCTGGTAACAGATATCAAGG 446
Db        558 TACCTGCACTGGCTGGTCACTGATATTCCGG 588


RESULT 12
AAD42243
ID   AAD42243 standard; cDNA; 1191 BP.
XX
AC   AAD42243;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Corn FT homologue cDNA from clone p0081.chcad07r.
XX
KW   Floral developmental protein; flowering locus T; APETALA3; transgenic;
KW   FT; AP3; transgenic plant; fertility; flower development; gene mapping;
KW   sterility; plant growth; inflorescence architecture; plant morphology;
KW   tissue culture; cell division; corn; gene; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             175. .708
FT                   /*tag=  a
FT                   /product= "Corn FT homologue protein"
XX
PN   WO200244390-A2.
XX
PD   06-JUN-2002.
XX
PF   21-NOV-2001; 2001WO-US043750.
XX
PR   28-NOV-2000; 2000US-0253415P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon EB,  Cahoon RE,  Klein TM,  Rafalski AJ,  Sakai H;
XX
DR   WPI; 2002-547703/58.
DR   P-PSDB; AAE25741.
XX
PT   New floral developmental polypeptide having flowering locus T or Ap3
PT   homolog activity, useful for immunological screening of cDNA expression
PT   libraries.
XX
PS   Claim 6; Page 60; 88pp; English.
XX
CC   The present invention relates to novel floral developmental proteins,
CC   more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
CC   proteins and polynucleotides encoding such proteins. Floral developmental
CC   polynucleotides are useful for transforming cells or for producing plants
CC   by transforming the plant cells with the polynucleotides and regenerating
CC   the plants from the transformed plant cells. Sequences of the invention
CC   are useful for immunological screening of cDNA expression libraries. They
CC   are also useful for creating transgenic plants. Polynucleotides of the
CC   invention are used as probes for genetically and physically mapping the
CC   genes that they are a part of and as markers for traits linked to those
CC   genes. AP3 homologues may be useful for engineering plant sterility or
CC   fertility, flower development and morphology. FT or TFL1 homologues are
CC   useful for engineering flowering time, plant growth rate, inflorescence
CC   architecture, tissue culture morphology and rate of cell division to
```

```
CC   enhance transformation. The present sequence is corn FT homologue cDNA
XX
SQ   Sequence 1191 BP; 280 A; 317 C; 344 G; 250 T; 0 U; 0 Other;

  Query Match             5.4%;  Score 48.2;  DB 1;  Length 1191;
  Best Local Similarity   60.2%;  Pred. No. 0;
  Matches   80;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
              |||| |  ||| || ||  |||  | |      |  |   ||| | ||| ||||||||||
Db        326 AGCCCAGGGTCGAGGTCGGGGGACCTGACATGAGGACCTTCTACACCCTCGTGATGGTGG 385

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
              | || ||||| || |||  |   || || |  |  ||    |    ||| |||||||| |
Db        386 ACCCGGATGCTCCGAGCCCAAGCGACCCGAACCTTAGGGAGTACCTACACTGGCTGGTGA 445

Qy        435 CAGATATCAAGGG 447
              | |||||   |||
Db        446 CGGATATTCCGGG 458


Search completed: February 22, 2005, 12:43:20
Job time : 3 secs
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; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; Hillman, Jennifer
; Corley, Neil
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,401
; FILING DATE: 11-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,820
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0379 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTUT12
; CLONE: 3126479
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-879-401-4

Query Match 96.5%; Score 858.9; DB 1; Length 903;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 873; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy          2 AGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCT 61
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||| ||||
Db          1 AGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCT 60

Qy         62 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 120

Qy        122 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 180

Qy        182 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 240

Qy        242 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 300

Qy        302 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 360
```

```
Qy        362 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 420

Qy        422 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAG 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAG 480

Qy        482 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 540

Qy        542 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 600

Qy        602 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 660

Qy        662 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 720

Qy        722 AGGGCCAGCGAGCCCAAGCACAAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 781
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        721 AGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        781 TTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCC 840

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||||||||||||||| |||||||||
Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAAA 880
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Search completed: February 22, 2005, 12:49:27
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 12:49:26 ; Search time 1 Seconds
(without alignments)
3.266 Million cell updates/sec

Title: US-10-035-958-60
Perfect score: 890
Sequence: 1 AAGTACTTGTGTCCGGGTGG.....TAAAAAAAAAAATCATCAAA 890

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 1835 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : k035rnpb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	865.7	97.3	932	1	US-10-003-152-1	Sequence 1, Appli
2	858.9	96.5	903	1	US-09-879-401-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-003-152-1
; Sequence 1, Application US/10003152
; Publication No. US20020151494A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20020151494A1el Amino Acid Sequences for Human Semaphorin-L
; FILE REFERENCE: 15966-554 Cura-54 CON-S12
; CURRENT APPLICATION NUMBER: US/10/003,152
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)..(793)
US-10-003-152-1

Query Match 97.3%; Score 865.7; DB 1; Length 932;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 881; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy    1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||| |||
Db   25 AAGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCC 84

Qy   61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 144

Qy  121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  145 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 204

Qy  181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
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Db  205 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 264

Qy  241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
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Db  265 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 324

Qy  301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
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Qy  361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
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Db  385 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 444

Qy  421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
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Db  445 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCA 504

Qy  481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
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Qy  541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
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Qy  601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660
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Db  625 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGC 684

Qy  661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
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Qy  721 AAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGG 779
          |||||||||||||||||||||| ||||||||| |||||||||||||||||||||||||
Db  745 AAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGG 804

Qy  780 CTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCC 839
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  805 CTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCC 864

Qy  840 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCATCAA 889
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Db  865 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCATCCA 914
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RESULT 2
US-09-879-401-4
; Sequence 4, Application US/09879401
; Publication No. US20030119730A1

GenCore version 5.1.6
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cleic - nucleic search, using sw model

on: February 22, 2005, 12:32:47 ; Search time 0.001 Seconds
(without alignments)
626.560 Million cell updates/sec

le: US-10-035-958-60
fect score: 890
uence: 1 AAGTACTTGTGTCCGGGTGG.....TAAAAAAAAAAATCATCAAA 890

oring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

earched: 1 seqs, 352 residues

otal number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : k035rge:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	330.5	37.1	352	1	G27363	ACCESSION:G27363

ALIGNMENTS

RESULT 1
G27363/c
LOCUS G27363 352 bp DNA linear STS 28-JUN-1996
DEFINITION human STS SHGC-31033, sequence tagged site.
ACCESSION G27363
VERSION G27363.1 GI:1396086
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 352)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: TTGGAAAAGAAGGGGTTCTG
Primer B: AAGCACAAAAACCAGGCG
STS size: 133
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived :
-- Washington University/Merck EST sequence.
FEATURES Location/Qualifiers
source 1. .352
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="8"
STS 4. .136
primer_bind 4. .23
primer_bind complement(119. .136)

Query Match 37.1%; Score 330.5; DB 1; Length 352;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 344; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy        521 AGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTC 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 AGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTC 293

Qy        581 CTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTC 640
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        292 CTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTC 233

Qy        641 CACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCA 700
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Db        232 CACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCA 173

Qy        701 ACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATA 759
              |||||||||||||||||| |||||||||||||||||||||| |||||||||| ||||||
Db        172 ACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATA 113

Qy        760 GCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGA 819
              |||||||||||||||| | |||||||||||||||||||||||||||||| |||||||||
Db        112 GCTGCCTGCTAGATAGNCCGCTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGA 53

Qy        820 CGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAAT 870
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Db         52 CGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAAT 2
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Search completed: February 22, 2005, 12:32:47
Job time : 0.001 secs

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Qy      181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
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Db      192 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 251

Qy      241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      252 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 311

Qy      301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
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Db      312 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGTACGGCGCAACCTATAT 371

Qy      361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      432 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 491

Qy      481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      492 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 551

Qy      541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      552 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 611

Qy      601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      612 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGC 671

Qy      661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      672 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGA 731

Qy      721 AAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGG 779
            |||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||||
Db      732 AAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGG 791

Qy      780 CTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCC 839
            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      792 CTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCC 851

Qy      840 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAA 889
            ||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db      852 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCCA 901
```

RESULT 2
AAA15582
ID AAA15582 standard; cDNA; 903 BP.
XX
AC AAA15582;
XX
DT 01-AUG-2000 (first entry)
XX
DE Human phospholipid binding protein 2, PLBP2 gene.
XX
KW Human; phospholipid binding protein; PLBP2; foetal development disorder;
KW reproduction disorder; cell proliferation disorder; immune response;
KW autoimmune disorder; AIDS; infertility; cytostatic; immunosuppressive;
KW gene therapy; hereditary neuropathy;
KW phosphatidylethanolamine binding protein D1; PE-BP D1; ss.
XX
OS Homo sapiens.

Key	Location/Qualifiers
CDS	88. .771
	/*tag= a
	/product= "Human PLBP2"

PN US6063767-A.
XX
PD 16-MAY-2000.
XX
PF 09-DEC-1998; 98US-00208718.
XX
PR 28-OCT-1997; 97US-00958820.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Corley NC, Shah P, Lal P, Hillman JL;
XX
DR WPI; 2000-375529/32.
DR P-PSDB; AAY94263.
XX
PT New purified phospholipid binding proteins 1 and 2 useful for diagnosing,
PT treating or preventing diseases disorders associated with fetal
PT development, reproduction, cell proliferation, and the immune response.
XX
PS Example 5; Fig 2; 37pp; English.
XX
CC The present sequence is the phospholipid binding protein 2 (PLBP2) gene.
CC This gene is expressed in lung, prostate and heart tissues. Also, the
CC protein is expressed in foetal tumour tissues. PLBP2 may be used for the
CC diagnosis, prevention, or treatment of disorders associated with foetal
CC development (e.g. hereditary neuropathies), reproduction (e.g.
CC infertility), cell proliferation (e.g. cancers), and the immune response
CC (AIDS). PLBP2 antibodies may also be developed for potential drug
CC screening or to quantitate PLBP2 gene expression in biopsied tissues. The
CC PLBP2 gene may be administered for gene therapy of disorders associated
CC with PLBP2. PLBP2 has high homology with the phosphatidylethanolamine
CC binding protein D1, PE-BP D1, of Onchocerca volvulus. PE-BP DI is thought
CC to play a role in transport or signal mechanisms between membranes and
CC the cytoplasm
XX
SQ Sequence 903 BP; 222 A; 251 C; 242 G; 188 T; 0 U; 0 Other;

Query Match 96.5%; Score 858.9; DB 1; Length 903;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 873; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy        2 AGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCT 61
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||| ||||
Db        1 AGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCT 60

Qy       62 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 120

Qy      122 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 180

Qy      182 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 240

Qy      242 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 300

Qy      302 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 360

Qy      362 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 420

Qy      422 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAG 481
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      421 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAG 480
```

```
Qy        482 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 541
Db        481 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 540

Qy        542 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 601
Db        541 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 600

Qy        602 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 661
Db        601 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 660

Qy        662 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 721
Db        661 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 720

Qy        722 AGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780
Db        721 AGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
Db        781 TTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCC 840

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAA 880
```

RESULT 3
ADK70378
ID ADK70378 standard; cDNA; 903 BP.
XX
AC ADK70378;
XX
DT 06-MAY-2004 (first entry)
XX
DE Respiratory disease differentially expressed cDNA #114.
XX
KW ds; gene; cytostatic; respiratory; antiasthmatic; gene therapy;
KW differential gene expression; respiratory disorder; lung cancer;
KW chronic obstructive pulmonary disease; emphysema; asthma.
XX
OS Homo sapiens.
XX
PN WO2003101283-A2.
XX
PD 11-DEC-2003.
XX
PF 02-JUN-2003; 2003WO-US017409.
XX
PR 04-JUN-2002; 2002US-0386005P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Rickert PK, Krasnow R;
XX
DR WPI; 2004-042945/04.
XX
PT New combination comprising cDNAs and proteins that are differentially
PT expressed in respiratory disorders, useful for diagnosing or treating
PT respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
PT diseases or asthma.
XX
PS Claim 1; SEQ ID NO 114; 343pp; English.
XX
CC The invention relates to cDNA sequences that are differentially expressed
CC in respiratory disorders or their complements or encoded proteins. The
CC cDNAs and proteins are useful for diagnosing, treating or monitoring
CC treatment of a subject with a respiratory disease including lung cancer,
CC chronic obstructive pulmonary diseases, emphysema or asthma. The protein
CC is also useful for screening molecules or compounds to identify at least
CC one ligand which specifically binds the protein. It is also useful for
CC preparing and purifying a polyclonal or monoclonal antibody. This
CC sequence corresponds to a cDNA of the invention.
XX
SQ Sequence 903 BP; 222 A; 251 C; 242 G; 188 T; 0 U; 0 Other;

Query Match   96.5%; Score 858.9; DB 1; Length 903;
Best Local Similarity   99.2%; Pred. No. 0;
Matches 873; Conservative   0; Mismatches   6; Indels   1; Gaps   1;

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Qy          2 AGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCT 61
Db          1 AGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCT 60

Qy         62 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 121
Db         61 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 120

Qy        122 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 181
Db        121 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 180

Qy        182 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 241
Db        181 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 240

Qy        242 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 301
Db        241 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 300

Qy        302 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 361
Db        301 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 360

Qy        362 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 421
Db        361 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 420

Qy        422 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAG 481
Db        421 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAG 480

Qy        482 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 541
Db        481 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 540

Qy        542 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 601
Db        541 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 600

Qy        602 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 661
Db        601 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 660

Qy        662 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 721
Db        661 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 720

Qy        722 AGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780
Db        721 AGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
Db        781 TTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCC 840

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAA 880
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RESULT 4
AAF94490
ID AAF94490 standard; cDNA; 897 BP.